

# SEQUENCE LISTING

<110> Svendsen, Allan  
Bisgard-Frantzen, Henrik  
Borchert, Torben Vedel

<120> Alpha-Amylase Mutants

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<140> 09/327,563

<141> 1999-06-08

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aagtgaagaa gcagagaggc tattgaataa atgagtagaa gcgccatata ggcgcttttc   240
tttggaaga aaatatagggg aaaatggtac ttgttaaaaa ttcggaatat ttatacaaca   300
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aac gac tcg gca tat ttg gct gaa cac ggt att act gcc gtc tgg att 546  
Asn Asp Ser Ala Tyr Leu Ala Glu His Gly Ile Thr Ala Val Trp Ile  
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ccc ccg gca tat aag gga acg agc caa gcg gat gtg ggc tac ggt gct 594  
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cat tcc cgc gac att aac gtt tac ggg gat gtg gtc atc aac cac aaa 738  
His Ser Arg Asp Ile Asn Val Tyr Gly Asp Val Val Ile Asn His Lys  
95 100 105

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Gly Gly Ala Asp Ala Thr Glu Asp Val Thr Ala Val Glu Val Asp Pro  
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gct gac cgc aac cgc gta att tca gga gaa cac cta att aaa gcc tgg 834  
Ala Asp Arg Asn Arg Val Ile Ser Gly Glu His Leu Ile Lys Ala Trp  
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Thr His Phe His Phe Pro Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys  
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Trp His Trp Tyr His Phe Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys  
155 160 165 170

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Tyr Asp His Pro Asp Val Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp  
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tat gcc aat gaa ctg caa ttg gac ggt ttc cgt ctt gat gct gtc aaa 1122  
Tyr Ala Asn Glu Leu Gln Leu Asp Gly Phe Arg Leu Asp Ala Val Lys  
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415 420 425

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Leu Ile Thr Asp Gly Pro Gly Gly Ala Lys Arg Met Tyr Val Gly Arg  
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Gln His Trp Arg Arg Leu Gln Asn Asp Ser Ala Tyr Leu Ala Glu His  
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Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Thr Ser Gln  
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Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu Phe  
85 90 95  
His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu Leu  
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Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn Val Tyr Gly  
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130 135 140  
Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val Ile Ser Gly  
145 150 155 160  
Glu His Leu Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg Gly  
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Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly Thr  
180 185 190  
Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys Phe Gln Gly  
195 200 205  
Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn Tyr Asp Tyr  
210 215 220  
Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala Ala Glu  
225 230 235 240  
Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu Asp Gly  
245 250 255  
Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Leu Arg Asp  
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Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met Phe Thr Val  
275 280 285  
Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu Asn  
290 295 300  
Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His Tyr Gln  
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Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met Arg Lys Leu  
325 330 335

Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser Val Thr Phe  
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 Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr Val  
 355 360 365  
 Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg Glu  
 370 375 380  
 Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys Gly  
 385 390 395 400  
 Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro Ile  
 405 410 415  
 Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr Phe  
 420 425 430  
 Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser Val  
 435 440 445  
 Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly Ala  
 450 455 460  
 Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His Asp  
 465 470 475 480  
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 atcagacagg gtattttta tgctgtccag actgtccgct gtgtaaaaat aaggaataaa 180  
 ggggggttgt tattatttta ctgatatgta aatatataatt tgtataagaa aatgagaggg 240  
 agaggaaac atg att caa aaa cga aag cgg aca gtt tcg ttc aga ctt gtg 291  
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Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser			
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Asp Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu			
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agc caa tcc gat aac gga tac gga cct tat gat ttg tat gat tta gga 531			
Ser Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly			
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Glu Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser			
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Tyr Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu			
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Asp Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr			
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Ser Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly			
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Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp			
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Arg Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly  
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aac tat gac tat tta atg tat gct gat gtt gac tac gac cac cct gat 963  
Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp  
195 200 205

gtc gtg gca gag aca aaa aaa tgg ggt atc tgg tat gcg aat gaa ctg 1011  
Val Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu  
210 215 220

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Ser Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser  
225 230 235

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Phe Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu  
240 245 250 255

atg ttt acg gtt gcg gag tat tgg cag aat aat gcc ggg aaa ctc gaa 1155  
Met Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu Glu  
260 265 270

aac tac ttg aat aaa aca agc ttt aat caa tcc gtg ttt gat gtt ccg 1203  
Asn Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val Pro  
275 280 285

ctt cat ttc aat tta cag gcg gct tcc tca caa gga ggc gga tat gat 1251  
Leu His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr Asp  
290 295 300

atg agg cgt ttg ctg gac ggt acc gtt gtg tcc agg cat ccg gaa aag 1299  
Met Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu Lys  
305 310 315

gcg gtt aca ttt gtt gaa aat cat gac aca cag ccg gga cag tca ttg 1347  
Ala Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser Leu  
320 325 330 335



gaa teg aca gtc caa act tgg ttt aaa ccg ctt gca tac gcc ttt att 1395  
Glu Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile  
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Gly Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn  
370 375 380

ata gag ccg att tta aaa gcg cgt aag gag tac gca tac ggg ccc cag 1539  
Ile Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln  
385 390 395

cac gat tat att gac cac ccg gat gtg atc gga tgg acg agg gaa ggt 1587  
His Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly  
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Ser Asp Gly Trp Gly Glu Phe His Val Asn Asp Gly Ser Val Ser Ile  
465 470 475

tat gtt cag aaa taaggtaata aaaaaacacc tccaagctga gtgcgggtat 1831  
Tyr Val Gln Lys  
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catgtctgat tttgtataa tcaacaggca cggagccgga atctttcgcc ttggaaaaat 2011  
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Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp Ile  
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Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser Gln  
65 70 75 80  
Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu Phe  
85 90 95  
Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu Leu  
100 105 110  
Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr Gly  
115 120 125  
Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp Val  
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Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser Glu  
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Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg Gly  
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Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn Tyr  
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Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val Val  
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Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe Leu  
260 265 270  
Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met Phe  
275 280 285  
Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu Glu Asn Tyr  
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305            310            315            320  
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 Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu Lys Ala Val  
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 Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr  
           370            375            380  
 Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr  
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 Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile Glu  
           405            410            415  
 Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln His Asp  
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 Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp Ser  
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 Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly  
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 Tyr Asp Ile Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser Asp  
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 Val Leu Thr Phe His Arg  
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 Thr Leu Trp Thr Lys Val Ala Asn Glu Ala Asn Asn Leu Ser Ser Leu  
 25 30 35

ggc atc acc gct ctt tgg ctg ccg ccc gct tac aaa gga aca agc cgc 413  
 Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala Tyr Lys Gly Thr Ser Arg  
 40 45 50

agc gac gta ggg tac gga gta tac gac ttg tat gac ctc gcc gaa ttc 461  
 Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu Tyr Asp Leu Gly Glu Phe  
 55 60 65

aat caa aaa ggg acc gtc cgc aca aaa tac gga aca aaa gct caa tat 509  
 Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ala Gln Tyr  
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ctt caa gcc att caa gcc gcc cac gcc gct gga atg caa gtg tac gcc 557  
 Leu Gln Ala Ile Gln Ala Ala His Ala Ala Gly Met Gln Val Tyr Ala  
 85 90 95 100

gat gtc gtg ttc gac cat aaa ggc ggc gct gac ggc acg gaa tgg gtg 605  
 Asp Val Val Phe Asp His Lys Gly Gly Ala Asp Gly Thr Glu Trp Val  
 105 110 115

gac gcc gtc gaa gtc aat ccg tcc gac cgc aac caa gaa atc tcg gcc 653  
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Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe Asp Phe Pro Gly Arg Gly  
135 140 145

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150 155 160

gat tgg gac gaa agc cga aaa ttg agc cgc att tac aaa ttc cgc ggc 797  
Asp Trp Asp Glu Ser Arg Lys Leu Ser Arg Ile Tyr Lys Phe Arg Gly  
165 170 175 180

atc ggc aaa gcg tgg gat tgg gaa gta gac acg gaa aac gga aac tat 845  
Ile Gly Lys Ala Trp Asp Trp Glu Val Asp Thr Glu Asn Gly Asn Tyr  
185 190 195

gac tac tta atg tat gcc gac ctt gat atg gat cat ccc gaa gtc gtg 893  
Asp Tyr Leu Met Tyr Ala Asp Leu Asp Met Asp His Pro Glu Val Val  
200 205 210

acc gag ctg aaa aac tgg ggg aaa tgg tat gtc aac aca acg aac att 941  
Thr Glu Leu Lys Asn Trp Gly Lys Trp Tyr Val Asn Thr Thr Asn Ile  
215 220 225

gat ggg ttc cgg ctt gat gcc gtc aag cat att aag ttc agt ttt ttt 989  
Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Phe  
230 235 240

cct gat tgg ttg tcg tat gtg cgt tct cag act ggc aag ccg cta ttt 1037  
Pro Asp Trp Leu Ser Tyr Val Arg Ser Gln Thr Gly Lys Pro Leu Phe  
245 250 255 260

acc gtc ggg gaa tat tgg agc tat gac atc aac aag ttg cac aat tac 1085  
Thr Val Gly Glu Tyr Trp Ser Tyr Asp Ile Asn Lys Leu His Asn Tyr  
265 270 275

att acg aaa aca gac gga acg atg tct ttg ttt gat gcc ccg tta cac 1133  
Ile Thr Lys Thr Asp Gly Thr Met Ser Leu Phe Asp Ala Pro Leu His  
280 285 290

aac aaa ttt tat acc gct tcc aaa tca ggg ggc gca ttt gat atg cgc 1181  
Asn Lys Phe Tyr Thr Ala Ser Lys Ser Gly Gly Ala Phe Asp Met Arg  
295 300 305

acg tta atg acc aat act ctc atg aaa gat caa ccg aca ttg gcc gtc 1229

Thr Leu Met Thr Asn Thr Leu Met Lys Asp Gln Pro Thr Leu Ala Val  
310 315 320

acc ttc gtt gat aat cat gac acc gaa ccc ggc caa gcg ctg cag tca 1277  
Thr Phe Val Asp Asn His Asp Thr Glu Pro Gly Gln Ala Leu Gln Ser  
325 330 335 340

tgg gtc gac cca tgg ttc aaa ccg ttg gct tac gcc ttt att cta act 1325  
Trp Val Asp Pro Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr  
345 350 355

cgg cag gaa gga tac ccg tgc gtc ttt tat ggt gac tat tat ggc att 1373  
Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr Gly Asp Tyr Tyr Gly Ile  
360 365 370

cca caa tat aac att cct tcg ctg aaa agc aaa atc gat ccg ctc ctc 1421  
Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser Lys Ile Asp Pro Leu Leu  
375 380 385

atc gcg cgc agg gat tat gct tac gga acg caa cat gat tat ctt gat 1469  
Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln His Asp Tyr Leu Asp  
390 395 400

cac tcc gac atc atc ggg tgg aca agg gaa ggg ggc act gaa aaa cca 1517  
His Ser Asp Ile Ile Gly Trp Thr Arg Glu Gly Gly Thr Glu Lys Pro  
405 410 415 420

gga tcc gga ctg gcc gca ctg atc acc gat ggg ccg gga gga agc aaa 1565  
Gly Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly Ser Lys  
425 430 435

tgg atg tac gtt ggc aaa caa cac gct gga aaa gtg ttc tat gac ctt 1613  
Trp Met Tyr Val Gly Lys Gln His Ala Gly Lys Val Phe Tyr Asp Leu  
440 445 450

acc ggc aac cgg agt gac acc gtc acc atc aac agt gat gga tgg ggg 1661  
Thr Gly Asn Arg Ser Asp Thr Val Thr Ile Asn Ser Asp Gly Trp Gly  
455 460 465

gaa ttc aaa gtc aat ggc ggt tcg gtt tcg gtt tgg gtt cct aga aaa 1709  
Glu Phe Lys Val Asn Gly Gly Ser Val Ser Val Trp Val Pro Arg Lys  
470 475 480

acg acc gtt tct acc atc gct cgg ccg atc aca acc cga ccg tgg act 1757  
Thr Thr Val Ser Thr Ile Ala Arg Pro Ile Thr Thr Arg Pro Trp Thr

ggt gaa ttc gtc cgt tgg acc gaa cca cgg ttg gtg gca tgg cct 1802  
Gly Glu Phe Val Arg Trp Thr Glu Pro Arg Leu Val Ala Trp Pro  
505 510 515

tgatgcctgc ga 1814

<210> 6  
<211> 549  
<212> PRT  
<213> B. stearothermophilus

<400> 6

Val Leu Thr Phe His Arg Ile Ile Arg Lys Gly Trp Met Phe Leu Leu  
1 5 10 15

Ala Phe Leu Leu Thr Val Ser Leu Phe Cys Pro Thr Gly Gln Pro Ala  
20 25 30

Lys Ala Ala Ala Pro Phe Asn Gly Thr Met Met Gln Tyr Phe Glu Trp  
35 40 45

Tyr Leu Pro Asp Asp Gly Thr Leu Trp Thr Lys Val Ala Asn Glu Ala  
50 55 60

Asn Asn Leu Ser Ser Leu Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala  
65 70 75 80

Tyr Lys Gly Thr Ser Arg Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu  
85 90 95

Tyr Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr  
100 105 110

Gly Thr Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala Ala His Ala Ala  
115 120 125

Gly Met Gln Val Tyr Ala Asp Val Val Phe Asp His Lys Gly Gly Ala  
130 135 140

Asp Gly Thr Glu Trp Val Asp Ala Val Glu Val Asn Pro Ser Asp Arg  
145 150 155 160

Asn Gln Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe  
165 170 175

Asp Phe Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp  
180 185 190

Tyr His Phe Asp Gly Val Asp Trp Asp Glu Ser Arg Lys Leu Ser Arg  
195 200 205

Ile Tyr Lys Phe Arg Gly Ile Gly Lys Ala Trp Asp Trp Glu Val Asp  
210 215 220

Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Leu Asp Met  
225 230 235 240

Asp His Pro Glu Val Val Thr Glu Leu Lys Asn Trp Gly Lys Trp Tyr

245            250            255  
 Val Asn Thr Thr Asn Ile Asp Gly Phe Arg Leu Asp Ala Val Lys His  
 260            265            270  
 Ile Lys Phe Ser Phe Phe Pro Asp Trp Leu Ser Tyr Val Arg Ser Gln  
 275            280            285  
 Thr Gly Lys Pro Leu Phe Thr Val Gly Glu Tyr Trp Ser Tyr Asp Ile  
 290            295            300  
 Asn Lys Leu His Asn Tyr Ile Thr Lys Thr Asp Gly Thr Met Ser Leu  
 305            310            315            320  
 Phe Asp Ala Pro Leu His Asn Lys Phe Tyr Thr Ala Ser Lys Ser Gly  
 325            330            335  
 Gly Ala Phe Asp Met Arg Thr Leu Met Thr Asn Thr Leu Met Lys Asp  
 340            345            350  
 Gln Pro Thr Leu Ala Val Thr Phe Val Asp Asn His Asp Thr Glu Pro  
 355            360            365  
 Gly Gln Ala Leu Gln Ser Trp Val Asp Pro Trp Phe Lys Pro Leu Ala  
 370            375            380  
 Tyr Ala Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr  
 385            390            395            400  
 Gly Asp Tyr Tyr Gly Ile Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser  
 405            410            415  
 Lys Ile Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr  
 420            425            430  
 Gln His Asp Tyr Leu Asp His Ser Asp Ile Ile Gly Trp Thr Arg Glu  
 435            440            445  
 Gly Gly Thr Glu Lys Pro Gly Ser Gly Leu Ala Ala Leu Ile Thr Asp  
 450            455            460  
 Gly Pro Gly Gly Ser Lys Trp Met Tyr Val Gly Lys Gln His Ala Gly  
 465            470            475            480  
 Lys Val Phe Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile  
 485            490            495  
 Asn Ser Asp Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser  
 500            505            510  
 Val Trp Val Pro Arg Lys Thr Thr Val Ser Thr Ile Ala Arg Pro Ile  
 515            520            525  
 Thr Thr Arg Pro Trp Thr Gly Glu Phe Val Arg Trp Thr Glu Pro Arg  
 530            535            540  
 Leu Val Ala Trp Pro  
 545

<210> 7

<211> 31

<212> DNA

<213> Artificial Sequence



<220>

<223> Mutagenesis primer

<400> 7

ggtcgtaggc accgtagccc caatccgctt g

31

<210> 8

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Mutagenesis primer

<400> 8

ggtcgtaggc accgtagccc caatcccatt ggctcg

36

<210> 9

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Mutagenesis Primer

<400> 9

ctgtgactgg tgagtactca accaagtc

28

<210> 10

<211> 478

<212> PRT

<213> A. oryzae

<400> 10

Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr Phe Leu Leu Thr

1 5 10 15

Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala Thr Cys Asn Thr

20 25 30

Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly Ile Ile Asp Lys

35 40 45

Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro

50 55 60

Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly Asp Ala Tyr His

65 70 75 80

Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu Asn Tyr Gly Thr

85	90	95
Ala Asp Asp Leu Lys	Ala Leu Ser Ser	Ala Leu His Glu Arg Gly Met
100	105	110
Tyr Leu Met Val Asp	Val Val Ala Asn His	Met Gly Tyr Asp Gly Ala
115	120	125
Gly Ser Ser Val Asp	Tyr Ser Val Phe Lys	Pro Phe Ser Ser Gln Asp
130	135	140
Tyr Phe His Pro Phe	Cys Phe Ile Gln Asn	Tyr Glu Asp Gln Thr Gln
145	150	155
Val Glu Asp Cys Trp	Leu Gly Asp Asn Thr	Val Ser Leu Pro Asp Leu
165	170	175
Asp Thr Thr Lys Asp	Val Val Lys Asn Glu	Trp Tyr Asp Trp Val Gly
180	185	190
Ser Leu Val Ser Asn	Tyr Ser Ile Asp Gly	Leu Arg Ile Asp Thr Val
195	200	205
Lys His Val Gln Lys	Asp Phe Trp Pro Gly	Tyr Asn Lys Ala Ala Gly
210	215	220
Val Tyr Cys Ile Gly	Glu Val Leu Asp Gly	Asp Pro Ala Tyr Thr Cys
225	230	235
Pro Tyr Gln Asn Val	Met Asp Gly Val Leu	Asn Tyr Pro Ile Tyr Tyr
245	250	255
Pro Leu Leu Asn Ala	Phe Lys Ser Thr Ser	Gly Ser Met Asp Asp Leu
260	265	270
Tyr Asn Met Ile Asn	Thr Val Lys Ser Asp	Cys Pro Asp Ser Thr Leu
275	280	285
Leu Gly Thr Phe Val	Glu Asn His Asp Asn	Pro Arg Phe Ala Ser Tyr
290	295	300
Thr Asn Asp Ile Ala	Leu Ala Lys Asn Val	Ala Ala Phe Ile Ile Leu
305	310	315
Asn Asp Gly Ile Pro	Ile Ile Tyr Ala Gly	Gln Glu Gln His Tyr Ala
325	330	335
Gly Gly Asn Asp Pro	Ala Asn Arg Glu Ala	Thr Trp Leu Ser Gly Tyr
340	345	350
Pro Thr Asp Ser Glu	Leu Tyr Lys Leu Ile	Ala Ser Ala Asn Ala Ile
355	360	365
Arg Asn Tyr Ala Ile	Ser Lys Asp Thr Gly	Phe Val Thr Tyr Lys Asn
370	375	380
Trp Pro Ile Tyr Lys	Asp Asp Ile Thr Ile	Ala Met Arg Lys Gly Thr
385	390	395
Asp Gly Ser Gln Ile	Val Thr Ile Leu Ser	Asn Lys Gly Ala Ser Gly
405	410	415
Asp Ser Tyr Thr Leu	Ser Leu Ser Gly Ala	Gly Tyr Thr Ala Gly Gln
420	425	430
Gln Leu Thr Glu Val	Ile Gly Cys Thr Thr	Val Thr Val Gly Ser Asp
435	440	445

Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro Arg Val Leu Tyr  
 450                455                460  
 Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser Ser Ser  
 465                470                475

<210> 11  
 <211> 1458  
 <212> DNA  
 <213> Bascillius

<220>  
 <221> CDS  
 <222> (1)...(1455)

<400> 11  
 cat cat aat gga aca aat ggt act atg atg caa tat ttc gaa tgg tat    48  
 His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr  
 1                5                10                15

ttg cca aat gac ggg aat cat tgg aac agg ttg agg gat gac gca gct    96  
 Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala  
 20                25                30

aac tta aag agt aaa ggg ata aca gct gta tgg atc cca cct gca tgg    144  
 Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp  
 35                40                45

aag ggg act tcc cag aat gat gta ggt tat gga gcc tat gat tta tat    192  
 Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr  
 50                55                60

gat ctt gga gag ttt aac cag aag ggg acg gtt cgt aca aaa tat gga    240  
 Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly  
 65                70                75                80

aca cgc aac cag cta cag gct gcg gtg acc tct tta aaa aat aac ggc    288  
 Thr Arg Asn Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly  
 85                90                95

att cag gta tat ggt gat gtc gtc atg aat cat aaa ggt gga gca gat    336  
 Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp  
 100                105                110

ggt acg gaa att gta aat gcg gta gaa gtg aat cgg agc aac cga aac    384  
 Gly Thr Glu Ile Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn

115	120	125	
cag gaa acc tca gga gag tat gca ata gaa gcg tgg aca aag ttt gat    432			
Gln Glu Thr Ser Gly Glu Tyr Ala Ile Glu Ala Trp Thr Lys Phe Asp			
130	135	140	
ttt cct gga aga gga aat aac cat tcc agc ttt aag tgg cgc tgg tat    480			
Phe Pro Gly Arg Gly Asn Asn His Ser Ser Phe Lys Trp Arg Trp Tyr			
145	150	155	160
cat ttt gat ggg aca gat tgg gat cag tca cgc cag ctt caa aac aaa    528			
His Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys			
165	170	175	
ata tat aaa ttc agg gga aca ggc aag gcc tgg gac tgg gaa gtc gat    576			
Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp			
180	185	190	
aca gag aat ggc aac tat gac tat ctt atg tat gca gac gtg gat atg    624			
Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met			
195	200	205	
gat cac cca gaa gta ata cat gaa ctt aga aac tgg gga gtg tgg tat    672			
Asp His Pro Glu Val Ile His Glu Leu Arg Asn Trp Gly Val Trp Tyr			
210	215	220	
acg aat aca ctg aac ctt gat gga ttt aga ata gat gca gtg aaa cat    720			
Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His			
225	230	235	240
ata aaa tat agc ttt acg aga gat tgg ctt aca cat gtg cgt aac acc    768			
Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr			
245	250	255	
aca ggt aaa cca atg ttt gca gtg gct gag ttt tgg aaa aat gac ctt    816			
Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu			
260	265	270	
ggt gca att gaa aac tat ttg aat aaa aca agt tgg aat cac tcg gtg    864			
Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His Ser Val			
275	280	285	
ttt gat gtt cct ctc cac tat aat ttg tac aat gca tct aat agc ggt    912			
Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly			
290	295	300	

ggt tat tat gat atg aga aat att tta aat ggt tct gtg gtg caa aaa 960  
Gly Tyr Tyr Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gln Lys  
305 310 315 320

cat cca aca cat gcc gtt act ttt gtt gat aac cat gat tct cag ccc 1008  
His Pro Thr His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro  
325 330 335

ggg gaa gca ttg gaa tcc ttt gtt caa caa tgg ttt aaa cca ctt gca 1056  
Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro Leu Ala  
340 345 350

tat gca ttg gtt ctg aca agg gaa caa ggt tat cct tcc gta ttt tat 1104  
Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr  
355 360 365

ggg gat tac tac ggt atc cca acc cat ggt gtt ccg gct atg aaa tct 1152  
Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser  
370 375 380

aaa ata gac cct ctt ctg cag gca cgt caa act ttt gcc tat ggt acg 1200  
Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr Gly Thr  
385 390 395 400

cag cat gat tac ttt gat cat cat gat att atc ggt tgg aca aga gag 1248  
Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu  
405 410 415

gga aat agc tcc cat cca aat tca ggc ctt gcc acc att atg tca gat 1296  
Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp  
420 425 430

ggt cca ggt ggt aac aaa tgg atg tat gtg ggg aaa aat aaa gcg gga 1344  
Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys Asn Lys Ala Gly  
435 440 445

caa gtt tgg aga gat att acc gga aat agg aca ggc acc gtc aca att 1392  
Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile  
450 455 460

aat gca gac gga tgg ggt aat ttc tct gtt aat gga ggg tcc gtt tcg 1440  
Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser  
465 470 475 480

gtt tgg gtg aag caa taa  
Val Trp Val Lys Gln  
485

1458

<210> 12  
<211> 485  
<212> PRT  
<213> Bascillius

<400> 12

His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr  
1 5 10 15  
Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala  
20 25 30  
Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp  
35 40 45  
Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr  
50 55 60  
Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly  
65 70 75 80  
Thr Arg Asn Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly  
85 90 95  
Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp  
100 105 110  
Gly Thr Glu Ile Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn  
115 120 125  
Gln Glu Thr Ser Gly Glu Tyr Ala Ile Glu Ala Trp Thr Lys Phe Asp  
130 135 140  
Phe Pro Gly Arg Gly Asn Asn His Ser Ser Phe Lys Trp Arg Trp Tyr  
145 150 155 160  
His Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys  
165 170 175  
Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp  
180 185 190  
Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met  
195 200 205  
Asp His Pro Glu Val Ile His Glu Leu Arg Asn Trp Gly Val Trp Tyr  
210 215 220  
Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His  
225 230 235 240  
Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr  
245 250 255  
Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu  
260 265 270

Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His Ser Val  
 275                      280                      285  
 Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly  
 290                      295                      300  
 Gly Tyr Tyr Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gln Lys  
 305                      310                      315                      320  
 His Pro Thr His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro  
 325                      330                      335  
 Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro Leu Ala  
 340                      345                      350  
 Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr  
 355                      360                      365  
 Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser  
 370                      375                      380  
 Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr Gly Thr  
 385                      390                      395                      400  
 Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu  
 405                      410                      415  
 Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp  
 420                      425                      430  
 Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys Asn Lys Ala Gly  
 435                      440                      445  
 Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile  
 450                      455                      460  
 Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser  
 465                      470                      475                      480  
 Val Trp Val Lys Gln  
 485

<210> 13  
 <211> 483  
 <212> PRT  
 <213> Bascillius

<400> 13  
 Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp  
 1                      5                      10                      15  
 Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp  
 20                      25                      30  
 Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser  
 35                      40                      45  
 Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu  
 50                      55                      60  
 Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu  
 65                      70                      75                      80

Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr  
           85              90              95  
 Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp  
         100              105              110  
 Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser  
         115              120              125  
 Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg  
         130              135              140  
 Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly  
 145              150              155              160  
 Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg  
         165              170              175  
 Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn  
         180              185              190  
 Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val  
         195              200              205  
 Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser  
         210              215              220  
 Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe  
 225              230              235              240  
 Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met  
         245              250              255  
 Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu Glu Asn  
         260              265              270  
 Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val Pro Leu  
         275              280              285  
 His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr Asp Met  
         290              295              300  
 Arg Lys Leu Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser  
 305              310              315              320  
 Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu  
         325              330              335  
 Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu  
         340              345              350  
 Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly  
         355              360              365  
 Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile  
         370              375              380  
 Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His  
 385              390              395              400  
 Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp  
         405              410              415  
 Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro  
         420              425              430  
 Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr



435            440            445  
 Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser  
 450            455            460  
 Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr  
 465            470            475            480  
 Val Gln Arg

<210> 14  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Substitution sequences

<400> 14  
 Ile Pro Thr His Ser Val  
 1            5

<210> 15  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

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